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OM nucleic - nucleic search, using sw model

Run on: February 14, 2005, 19:29:08 ; Search time 76 Seconds
(without alignments)

645.899 Million cell updates/sec

Title: SEQ1-191TC220

Perfect score: 30

Sequence: 1 taaatagctctgtatcatgctatgct 30

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUTS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29.6	98.7	30324	4 US-09-949-016-16037	Sequence 16037, A
2	21.8	72.7	264206	4 US-09-949-016-12731	Sequence 12731, A
3	21.8	72.7	264206	4 US-09-949-016-12731	Sequence 12731, A
4	21.8	72.7	264206	4 US-09-949-016-12731	Sequence 12731, A
5	21.2	70.7	29882	4 US-09-710-279-1385	Sequence 1385, Ap
6	21.2	70.7	3226	4 US-09-710-279-1385	Sequence 1385, Ap
7	20.8	69.3	138282	4 US-09-949-016-15307	Sequence 15307, A
8	20.2	67.3	35574	4 US-09-949-016-15307	Sequence 15307, A
9	20.2	67.3	35574	4 US-09-949-016-15307	Sequence 15307, A
10	20.2	67.3	35574	4 US-09-949-016-15307	Sequence 15307, A
11	20.2	67.3	165651	4 US-09-949-016-13032	Sequence 13032, A
12	20.2	67.3	165651	4 US-09-949-016-13032	Sequence 13032, A
13	20.2	67.3	253375	4 US-09-949-016-12849	Sequence 12849, A
14	19.8	66.0	457	4 US-09-949-016-12849	Sequence 12849, A
15	19.8	66.0	457	4 US-09-949-016-12849	Sequence 12849, A
16	19.6	65.3	1473	4 US-09-244-805-42	Sequence 42, Appl
17	19.6	65.3	311	4 US-09-513-999C-12912	Sequence 12912, A
18	19.6	65.3	373	4 US-09-513-999C-12912	Sequence 12912, A
19	19.6	65.3	501	4 US-09-513-999C-12912	Sequence 12912, A
20	19.6	65.3	601	4 US-09-949-016-13211	Sequence 13211, A
21	19.6	65.3	43192	4 US-09-949-016-15466	Sequence 15466, A
22	19.2	64.0	601	4 US-09-949-016-13058	Sequence 13058, A
23	19.2	64.0	1764	4 US-09-620-312D-548	Sequence 548, App
24	19.2	64.0	49487	4 US-09-949-016-15721	Sequence 15721, A
25	19.2	64.0	624	4 US-09-270-767-4747	Sequence 4747, Ap
26	19.2	64.0	624	4 US-09-270-767-4747	Sequence 4747, Ap
27	19.2	64.0	624	4 US-09-270-767-4747	Sequence 4747, Ap

28	19	63.3	3735	4 US-09-543-681A-2102	Sequence 2102, Ap
29	19	63.3	5488	4 US-09-949-016-17039	Sequence 17039, A
30	19	63.3	154626	4 US-09-949-016-14000	Sequence 14000, A
31	19	63.3	161124	4 US-09-949-016-11760	Sequence 11760, A
32	19	63.3	294836	4 US-09-949-016-15974	Sequence 15974, A
33	18.8	62.7	601	4 US-09-949-016-13211	Sequence 13211, A
34	18.8	62.7	13401	4 US-09-949-016-12239	Sequence 12239, A
35	18.8	62.7	13402	4 US-09-949-016-14595	Sequence 14595, A
36	18.8	62.7	43132	4 US-09-949-016-15466	Sequence 15466, A
37	18.6	62.0	437	4 US-09-949-016-185761	Sequence 185761, A
38	18.6	62.0	479	4 US-09-949-016-185757	Sequence 185757, A
39	18.6	62.0	601	4 US-09-949-016-88182	Sequence 88182, A
40	18.6	62.0	601	4 US-09-949-016-88845	Sequence 88845, A
41	18.6	62.0	601	4 US-09-949-016-154502	Sequence 154502, A
42	18.6	62.0	601	4 US-09-949-016-162928	Sequence 162928, A
43	18.6	62.0	601	4 US-09-949-016-195810	Sequence 195810, A
44	18.6	62.0	5900	4 US-09-949-016-14621	Sequence 14621, A
45	18.6	62.0	5993	3 US-09-383-630-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-949-016-16037
Sequence 16037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16037
LENGTH: 30324
TYPE: DNA
ORGANISM: Human
US-09-949-016-16037
Query Match 98.7%; Score 29.6; DB 4; Length 30324;
Best Local Similarity 96.7%; Pred. No. 0.0094;
Matches 29; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;
QY 1 TAAATAGCTCTGTATATGCTATATGCT 30
Db 25379 TAAATAGCTCTGTATATGCTATATGCT 25408
RESULT 2
US-09-949-016-52103/C
Sequence 52103, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
```

PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52103
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-52103

Query Match
Best Local Similarity 85.2%; Score 21.8; DB 4; Length 601;
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTTATATGCTATAT 27
DB 87 TATATATGCGCTATATATATGCTATAT 61

RESULT 3
US-09-949-016-12731
Sequence 12731, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12731
LENGTH: 264206
TYPE: DNA
ORGANISM: Human
US-09-949-016-12731

Query Match
Best Local Similarity 72.7%; Score 21.8; DB 4; Length 264206;
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTTATATGCTATAT 27
DB 135523 TATATATGCGCTATATATATGCTATAT 135549

RESULT 4
US-09-949-016-13249
Sequence 13249, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13249
LENGTH: 264304

TYPE: DNA
ORGANISM: Human
US-09-949-016-13249

Query Match
Best Local Similarity 72.7%; Score 21.8; DB 4; Length 264304;
Matches 23; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTTATATGCTATAT 27
DB 135523 TATATATGCGCTATATATATGCTATAT 135549

RESULT 5
US-09-710-279-3385
Sequence 3385, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3385
LENGTH: 2982
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-3385

Query Match
Best Local Similarity 70.7%; Score 21.2; DB 4; Length 2982;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATATGCTCTGTTATATGCTATATGCT 30
DB 42 AATGATCTCTGTAATATATGCTTATGCT 69

RESULT 6
US-09-710-279-4024
Sequence 4024, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4024
LENGTH: 3226
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-4024

Query Match
Best Local Similarity 70.7%; Score 21.2; DB 4; Length 3226;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 AATATGCTCTGTTATATGCTATATGCT 30

Db 3154 AATTGACTCTGTATATATGCTTATGCT 3181

RESULT 7
US-09-949-016-15307/c
; Sequence 15307, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15307
; LENGTH: 138282
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15307

Query Match 69.3%; Score 20.8; DB 4; Length 138282;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAAATGCTCTGTATATGCTATAT 27
Db 25404 ATATATGCTATATATATATGCTATAT 25379

RESULT 8
US-09-949-016-45077
; Sequence 45077, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45077
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-45077

Query Match 67.3%; Score 20.2; DB 4; Length 601;
Best Local Similarity 81.5%; Pred. No. 35;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATAT 27
Db 525 TTAATGCTCTCTTGTATATGCTATAT 551

RESULT 9

US-09-949-016-11843/c
; Sequence 11843, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11843
; LENGTH: 35574
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11843

Query Match 67.3%; Score 20.2; DB 4; Length 35574;
Best Local Similarity 81.5%; Pred. No. 67;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATAT 27
Db 164 TATATATGCGATGATATATATGCGATAT 138

RESULT 10
US-09-949-016-14511/c
; Sequence 14511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14511
; LENGTH: 35574
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14511

Query Match 67.3%; Score 20.2; DB 4; Length 35574;
Best Local Similarity 81.5%; Pred. No. 67;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATAT 27
Db 164 TATATATGCGATGATATATGCGATAT 138

RESULT 11
US-09-949-016-13032
; Sequence 13032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

```

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13032
; LENGTH: 165651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(165651)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13032
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Query Match      67.3%; Score 20.2; DB 4; Length 165651;
Best Local Similarity 81.5%; Pred. No. 86;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
      |||||:|||||:|||||:|||||:|||||
Db      67257 TTATATGCTCTTGTGTATATGCTATAT 67283
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RESULT 12
US-09-949-016-12849
; Sequence 12849, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12849
; LENGTH: 253375
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(253375)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12849
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```
Query Match      67.3%; Score 20.2; DB 4; Length 253375;
Best Local Similarity 81.5%; Pred. No. 92;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
      |||||:|||||:|||||:|||||:|||||
Db      5116 TATATATACTATGTATATATATATATAT 5142
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RESULT 13
US-09-949-016-12849/c
; Sequence 12849, Application US/09949016
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12849
; LENGTH: 253375
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(253375)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12849
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Query Match      67.3%; Score 20.2; DB 4; Length 253375;
Best Local Similarity 81.5%; Pred. No. 92;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
      |||||:|||||:|||||:|||||:|||||
Db      5457 TATATATACTATGTATATATATATATAT 5431
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RESULT 14
US-09-949-016-185760/c
; Sequence 185760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185760
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(457)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-185760
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Query Match      66.0%; Score 19.8; DB 4; Length 457;
Best Local Similarity 77.8%; Pred. No. 49;
Matches 21; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
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Db      308 TATATATATATGTATATATATATATATAT 282
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RESULT 15
US-09-244-805-42/c
; Sequence 42, Application US/09244805
; Patent No. 6699660
```

GENERAL INFORMATION:
; APPLICANT: Worley, Paul F.
; APPLICANT: Lanahan, Anthony
; APPLICANT: Goetz, Bernard
; APPLICANT: Heimlich, Holger
; APPLICANT: Kuner, Rohini
; APPLICANT: Scheek, Sigrid
; APPLICANT: Nikolich, Karoly
; APPLICANT: Zhukovski, Eugene
; TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 10496/004001
; CURRENT APPLICATION NUMBER: US/09/244,805
; CURRENT FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/074,518
; PRIOR FILING DATE: 1998-02-12
; PRIOR APPLICATION NUMBER: 60/074,135
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Eukaryote
US-09-244-805-42

Query Match 66.0%; Score 19.8; DB 4; Length 1473;
Best Local Similarity 84.0%; Pred. No. 59;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATGCTCTGRTATATGCTATATGCT 30
||| ||| : ||| ||| ||| |||
Db 647 ATGCTTGAATATCTGCTATATGCT 623

Search completed: February 14, 2005, 22:35:59
Job time : 80 secs

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OM nucleic - nucleic search, using SW model

Run on: February 14, 2005, 21:06:43 ; Search time 427 Seconds
(without alignments)
415.907 Million cell updates/sec

Title: SEQ1-191T0220
Perfect score: 30
Sequence: 1 taatatgctctgtatcatgctatgct 30

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	21.2	70.7	1273	ADCB7532
2	21.2	70.7	2982	AAH54021
3	21.2	70.7	3225	AAH54650
4	20.8	69.3	1781	ADRB7041
5	20.6	68.7	6291	ABL06646
6	20.6	68.7	32216	ABAI6118
7	20.6	68.7	39198	AAFS8067
8	20.6	68.7	46553	AAK81745
9	20.6	68.7	46553	AAK67926
10	20.6	68.7	59001	ADH54712
11	20.6	68.7	167932	ADL13501
12	20.4	68.0	4141	ABL05214
13	20.4	68.0	4164	ABL05338
14	20.2	67.3	2967	ABT18070
15	20.2	67.3	3423	ABT19884
16	20.2	67.3	15548	ABL34155
17	20.2	67.3	50000	ADCB0733
18	20.2	67.3	86592	AAZ22285
19	20.2	67.3	86592	AAI57236
20	20.2	67.3	86592	AAI60240

C	21	20	66.7	1571	2	AAZ06546	Aaz06546 Lazy 1a1
C	22	20	66.7	28198	10	ADG37080	Adg37080 Mouse pla
C	23	19.8	66.0	1473	2	AAZ28295	Aaz28295 Rat neuro
C	24	19.8	66.0	2852	4	ABLI0572	Abli0572 Drosophi1
C	25	19.8	66.0	12260	4	ABLO8874	Ablo8874 Drosophi1
C	26	19.6	65.3	311	3	AACO8837	Aaco8837 Human sec
C	27	19.6	65.3	373	3	AACO8838	Aaco8838 Human sec
C	28	19.6	65.3	384	8	ABX39244	Abx39244 Bovine ES
C	29	19.6	65.3	501	3	AAOC3846	Aaoc3846 Human sec
C	30	19.6	65.3	516	13	ADOS2128	Ados2128 Novel can
C	31	19.6	65.3	762	8	ACA27881	Acac27881 Prokaryot
C	32	19.6	65.3	1024	12	ADU40088	Adj40088 Plant cdn
C	33	19.6	65.3	1475	6	ABLI61912	Abli61912 Colon ade
C	34	19.6	65.3	1550	13	ACN38710	Acn38710 Tumour-as
C	35	19.6	65.3	1623	10	ADSO8797	Adso8797 Novel DNA
C	36	19.6	65.3	1717	5	ABV20232	Abv20232 Human pro
C	37	19.6	65.3	1717	5	ABV26061	Abv26061 Human pro
C	38	19.6	65.3	1891	10	ADBS3729	Adbs3729 Human pro
C	39	19.6	65.3	2076	6	ABK35195	Abk35195 Human cdn
C	40	19.6	65.3	4258	4	AAK68397	Aak68397 Human imm
C	41	19.6	65.3	203070	11	ACN44012	Acn44012 Mouse gen
C	42	19.4	64.7	26329	4	AAK42041	Aak42041 Genomic B
C	43	19.4	64.7	236246	12	ADQ97590	Adq97590 Mouse can
C	44	19.2	64.0	401	4	AAK95385	Aak95385 Human neu
C	45	19.2	64.0	401	4	AAK96878	Aak96878 Human neu

ALIGNMENTS

RESULT 1	ADCB7532	ADCB7532 standard; DNA; 1273 BP.
ID	ADCB7532	
XX	ADCB7532	
AC	ADCB7532	
DT	01-JAN-2004	(first entry)
XX		
DE	Human GPCR gene SEQ ID NO:1985.	
XX		
KW	de; gene; human; GPCR;	
KM	guanosine triphosphate-binding protein coupled receptor; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1270724-A2.	
XX		
PD	02-JAN-2003.	
XX		
PF	18-JUN-2002; 2002EP-00013517.	
XX		
PR	18-JUN-2001; 2001JP-00246789.	
XX		
PA	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.	
XX	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.	
XX		
PI	Suwa M, Asai K, Akiyama Y, Aburatani H;	
XX		
XX	WPI; 2003-315783/31.	
DR	P-PSDB; ADCB7533.	
XX		
PT	New polynucleotide, useful for preparing a composition for treating a	
PT	patient in need of increased or suppressed activity or expression of the	
PT	guanosine triphosphate-binding protein coupled receptor.	
XX		
PS	Claim 1; SEQ ID NO 1985; 28pp; English.	
XX		
CC	The invention relates to a novel polynucleotide encoding a guanosine	
CC	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of	
CC	the invention may have a use in gene therapy. The polynucleotide and	
CC	polypeptide are useful for preparing a composition for treating a patient	
CC	in need of increased or suppressed activity or expression of the	
CC	guanosine triphosphate-binding protein coupled receptor. The	

CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the
CC invention.
SQ Sequence 1273 BP; 444 A; 84 C; 126 G; 518 T; 0 U; 101 Other;
Query Match 70.7%; Score 21.2; DB 10; Length 1273;
Best Local Similarity 82.1%; Pred. No. 75;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 TAAATATGCTCTGTATATATGCTATATG 28
ID TATATATCTCTGTATATATATATATATG 882
Db 855 TATATATCTCTGTATATATATATATATG 882
RESULT 2
AAH54021
ID AAH54021 standard; DNA; 2982 BP.
XX
AC AAH54021;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3385.
XX
KM Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;
XX endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US030782.
XX
PR 09-NOV-1999; 99US-0164258P.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI kimmerly wj;
XX
DR WPI; 2001-316495/33.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis.
XX
PS Claim 8; Page 938-939; 2188pp; English.
XX
CC AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)
CC and (II) can have antibacterial activity and therefore can be used in
CC vaccination. The nucleic acids (I) may be used to produce the S.
CC epidermidis polypeptides (II) via the production of vectors containing
CC them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to AAH5098
CC represent oligonucleotide sequences and primers which are used in the
CC exemplification of the present invention. N.B. The present invention
CC specifically claims all the polynucleotide sequences given in the
CC sequence listing of the present specification, however the sequence
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given
CC in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present
CC for SEQ ID NO:4455 to 4464
XX
SQ Sequence 2982 BP; 753 A; 592 C; 434 G; 1203 T; 0 U; 0 Other;
Query Match 70.7%; Score 21.2; DB 4; Length 2982;
Best Local Similarity 82.1%; Pred. No. 82;

Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 AATATGCTCTGTATATATGCTATATGCT 30
ID AATGACTCTGTATATATGCTTTATGCT 69
Db 42 AATGACTCTGTATATATGCTTTATGCT 69
RESULT 3
AAH54660
ID AAH54660 standard; DNA; 3226 BP.
XX
AC AAH54660;
XX
DT 03-SEP-2001 (first entry)
XX
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4024.
XX
KM Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination;
XX endocarditis; ds.
XX
OS Staphylococcus epidermidis.
XX
PN WO200134809-A2.
XX
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000WO-US030782.
XX
PR 09-NOV-1999; 99US-0164258P.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI kimmerly wj;
XX
DR WPI; 2001-316495/33.
XX
PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
XX useful for vaccinating against infections, e.g. endocarditis.
XX
PS Claim 8; Page 1702-1703; 2188pp; English.
XX
CC AAH53970 represent nucleic acids (I) encoding polypeptides
CC (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I)
CC and (II) can have antibacterial activity and therefore can be used in
CC vaccination. The nucleic acids (I) may be used to produce the S.
CC epidermidis polypeptides (II) via the production of vectors containing
CC them which are used to produce hosts cells which express the
CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be
CC used to vaccinate subjects and to raise antibodies against the bacteria.
CC The polypeptides may also be used to assay for other inhibitors of their
CC activity and therefore identify compounds that may be used for the
CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
CC AAH5090 represent specifically claimed S. epidermidis genomic DNA
CC polynucleotide sequences from the present invention. AAH5091 to AAH5098
CC represent oligonucleotide sequences and primers which are used in the
CC exemplification of the present invention. N.B. The present invention
CC specifically claims all the polynucleotide sequences given in the
CC sequence listing of the present specification, however the sequence
CC listing only goes up to SEQ ID NO:4454 so even though sequences are given
CC in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present
CC for SEQ ID NO:4455 to 4464
XX
SQ Sequence 3226 BP; 727 A; 643 C; 518 G; 1338 T; 0 U; 0 Other;
Query Match 70.7%; Score 21.2; DB 4; Length 3226;
Best Local Similarity 82.1%; Pred. No. 82;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 AATATGCTCTGTATATATGCTATATGCT 30
ID AATGACTCTGTATATATGCTTTATGCT 3181
Db 3154 AATGACTCTGTATATATGCTTTATGCT 3181


```

RESULT 4
ID ADR07041 standard; cDNA; 1781 BP.
AC ADR07041;
DT 04-NOV-2004 (first entry)
XX
DE Full length human cDNA useful for creating neurological disease Seq 547.
XX
XX gene; ss; human; oligo-capping method; diagnostic marker; gene therapy;
XX osteoporosis; neurological disease; Alzheimer's disease;
XX Parkinson's disease; dementia; short memory; cancer;
XX sense or motor function; emotional reaction; fear response; panic;
XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
XX tranquiliser.
XX Homo sapiens.
XX EPI447413-A2.
XX
XX 18-AUG-2004.
XX
XX 12-FEB-2004; 2004BP-00003145.
XX
XX 14-FEB-2003; 2003JP-00102207.
XX
XX 09-MAY-2003; 2003JP-00131452.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Iisogai T, Yamamoto J, Nishikawa T, Isomo Y, Sugiyama T, Otsuki T,
XX Wakamatsu A, Ishii S, Negai K, Irie R;
XX WPI; 2004-583265/57.
XX
XX P-PSDB; ADR08997.
XX
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
XX Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
XX Claim 1, SEQ ID NO 547; 2686bp; English.
XX
XX This invention relates to novel, isolated full length human cDNA
XX molecules and the encoded proteins thereof. Specifically, it refers to
XX cDNA clones obtained by an oligo-capping method, where none of these
XX clones are identical to any known human mRNAs. The present invention
XX describes an immunoassay to identify agonists and antagonists, as well as
XX antibodies, antisense molecules and siRNAs that can all be used to bind
XX to and modulate expression of the cDNA molecules. As such, these
XX molecules are useful for diagnostic markers or therapeutic targets for
XX the various diseases or morbid states. In particular, they are useful in
XX gene therapy for treating osteoporosis, neurological disease, Alzheimer's
XX disease, Parkinson's disease, dementia, short memory and various cancers,
XX as well as for maintaining equilibrium of sense or motor function, and
XX for treating emotional reaction, fear response and panic. Accordingly,
XX they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
XX cyostatic and tranquiliser activities. This polynucleotide is a full
XX length human cDNA sequence of the invention. NOTE: This sequence is not
XX given in the sequence listing of the specification but can be obtained on
XX CD-ROM from the European Patent Office, Vienna Sub-office.
XX
XX Sequence 1781 BP; 443 A; 400 C; 417 G; 521 T; 0 U; 0 Other;
XX
Query Match 69.3%; Score 20.8; DB 13; Length 1781;
Best Local Similarity 84.6%; Pred. No. 1.1e+02;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 3 AATATGCTCTGTATATGCTATATG 28
XX |||||:|||||:|||||
Db 557 AATTGTTCTGTGTAATATCTATATG 582

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ID ABL06646 standard; cDNA; 6291 BP.
XX
XX ABL06646;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 14420.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX MO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX
XX P-PSDB; ABB62543.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
XX Claim 1, SEQ ID NO 14420; 21bp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL1840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at fcp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6291 BP; 1880 A; 1261 C; 1237 G; 1913 T; 0 U; 0 Other;
XX
Query Match 68.7%; Score 20.6; DB 4; Length 6291;
Best Local Similarity 79.3%; Pred. No. 1.5e+02;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX 2 AATATGCTCTGTATATGCTATATGCT 30
XX |||||:|||||:|||||
Db 2621 AATATGCTCTGTATATGCTATATGCT 2593

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RESULT 6
ID ABA16118 standard; DNA; 32216 BP.
AC ABA16118;
XX
XX 23-JAN-2002 (first entry)
DT
XX
XX Human nervous system related polynucleotide SEQ ID NO 8449.
DE
XX
XX Human; nootropic; neuroprotective; cyostatic; dermatological; virocidic;
XX immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX antiparkinsonian; antischizoling; antianaemic; anticholinergic; cancer;
XX antipneumatic; hepatoprotective; cerebroprotective; antiinflammatory;
XX antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX antiparasitic; cardiant; immune disorder; cardiovascular disorder;

```

KM neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX Homo sapiens.
XX WO200159063-A2.
XX 16-AUG-2001.
PF 17-JAN-2001; 2001WO-US001334.
XX
PR 31-JAN-2000; 2000US-0179066P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 11-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 14-JUL-2000; 2000US-0217496P.
PR 26-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 23-AUG-2000; 2000US-0227182P.
PR 30-AUG-2000; 2000US-0227009P.
PR 01-SEP-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 05-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
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PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
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PR 17-NOV-2000; 2000US-0246613P.
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PR 17-NOV-2000; 2000US-0249208P.
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PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251858P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX PT
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-541565/60.
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides.
XX PT useful for preventing, diagnosing and/or treating nervous system cancers
XX and metastases.
XX PS Disclosure; SEQ ID NO 8449; 1701bp + Sequence Listing; English.
XX CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
XX CC (ABA1678-ABA18001) useful for preventing, treating or ameliorating
XX CC medical conditions e.g. by protein or gene therapy. The genes are
XX CC isolated from a range of human tissues disclosed in the specification.
XX CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
XX CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
XX CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
XX CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
XX CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX CC infectious diseases such as viral, bacterial, fungal and parasitic
XX CC infections. Note: The sequence data for this patent did not form part of
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 32216 BP; 7528 A; 8136 C; 7649 G; 8903 T; 0 U; 0 Other;
XX
XX Query Match 68.7%; Score 20.6; DB 5; Length 32216;
XX Best Local Similarity 79.3%; Pred. No. 1.8e+02;
XX Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX 2 AAATATGCTCTGTATATGCTATATGCT 30
XX Db 22719 AAATATTCACGTGCTGCTATATGCT 22691
XX
XX RESULT 7
XX AAF58067/c
XX ID AAF58067 standard; DNA; 39198 BP.
XX XX
XX AAF58067;
XX XX
XX 26-APR-2001 (first entry)
XX XX
XX Human polyamine-modulated factor-1 PMF-1 gene.
XX XX
XX Human; polyamine-modulated factor-1; PMF-1; cancer; ds.
XX XX
XX Homo sapiens.
XX OS
XX WO200107610-A1.
XX PN
XX PD
XX 01-FEB-2001.
XX XX
XX 21-JUL-2000; 2000WO-US019994.
XX PF
XX 23-JUL-1999; 99US-0145347P.
XX PR
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX PA
XX Casero RA, Wang Y, Pegg AE;
XX PI
XX WPI; 2001-168553/17.
XX DR P-PSDB; AAB68986.
XX XX
XX New nucleic acid encoding human polyamine-modulated factor-1 for
XX PT regulating a polyamine-modulated factor-1-responsive, polyamine-dependent

PT gene in a cancerous cell.
XX XX
XX Claim 40; Fig 2; 61pp; English.
XX PS
XX CC The present invention provides the protein, coding and genomic sequences
XX CC of the human polyamine-modulated factor-1 protein (PMF-1). The sequences,
XX CC antibodies and analogues of the protein, are useful in the treatment
XX CC of cancer, via regulation of the spermidine/spermine N1-acetyltransferase
XX CC (SSAT) gene. The present sequence is the PMF-1 gene
XX XX
XX SQ Sequence 39198 BP; 9083 A; 9915 C; 9191 G; 11002 T; 0 U; 7 Other;
XX
XX Query Match 68.7%; Score 20.6; DB 5; Length 39198;
XX Best Local Similarity 79.3%; Pred. No. 1.8e+02;
XX Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
XX
XX 2 AAATATGCTCTGTATATGCTATATGCT 30
XX Db 28830 AAATATTCACGTGCTGCTATATGCT 28802
XX
XX RESULT 8
XX AAK81745/c
XX ID AAK81745 standard; DNA; 46553 BP.
XX XX
XX AAK81745;
XX AC
XX 07-NOV-2001 (first entry)
XX DT
XX XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36557.
XX DE
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX KW
XX Cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS
XX Homo sapiens.
XX PN
XX WO200157182-A2.
XX PD
XX 09-AUG-2001.
XX XX
XX 17-JAN-2001; 2001WO-US001354.
XX PF
XX 31-JAN-2000; 2000US-0179065P.
XX PR 04-FEB-2000; 2000US-0180628P.
XX PR 24-FEB-2000; 2000US-0184664P.
XX PR 02-MAR-2000; 2000US-0186350P.
XX PR 16-MAR-2000; 2000US-0189874P.
XX PR 17-MAR-2000; 2000US-0190076P.
XX PR 18-APR-2000; 2000US-0198123P.
XX PR 19-MAY-2000; 2000US-0205515P.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PR 28-JUN-2000; 2000US-0214886P.
XX PR 30-JUN-2000; 2000US-0215135P.
XX PR 07-JUL-2000; 2000US-0216647P.
XX PR 07-JUL-2000; 2000US-0216880P.
XX PR 11-JUL-2000; 2000US-0217487P.
XX PR 11-JUL-2000; 2000US-0217496P.
XX PR 14-JUL-2000; 2000US-0218290P.
XX PR 26-JUL-2000; 2000US-0220963P.
XX PR 26-JUL-2000; 2000US-0220964P.
XX PR 14-AUG-2000; 2000US-0224518P.
XX PR 14-AUG-2000; 2000US-0224519P.
XX PR 14-AUG-2000; 2000US-0225213P.
XX PR 14-AUG-2000; 2000US-0225214P.
XX PR 14-AUG-2000; 2000US-0225267P.
XX PR 14-AUG-2000; 2000US-0225267P.
XX PR 14-AUG-2000; 2000US-0225268P.
XX PR 14-AUG-2000; 2000US-0225270P.
XX PR 14-AUG-2000; 2000US-0225447P.
XX PR 14-AUG-2000; 2000US-0225757P.
XX PR 14-AUG-2000; 2000US-0225758P.
XX PR 14-AUG-2000; 2000US-0225759P.
XX PR 16-AUG-2000; 2000US-0226279P.

QY	2	AAATATGCTCTGTTATATGCTATATGCT	30
DB	37056	AAATATGCTCTGAGTCTGCTATATGCT	37028

RESULT 9
AK67926/c
ID AK67926 standard; DNA; 46553 BP.
XX
AC AK67926;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22738.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KM cytosolic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
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PR 30-JUN-2000; 2000US-0215135P.
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PR 01-SEP-2000; 2000US-0229287P.
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PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
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PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.

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PR 01-NOV-2000; 2000US-0244617P.
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PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
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PR 17-NOV-2000; 2000US-0249244P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
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PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCT INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 22738; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX SQ Sequence 46553 BP; 10776 A; 11618 C; 11092 G; 13067 T; 0 U; 0 Other;
Query Match 68.7%; Score 20.6; DB 4; Length 46553;
Best Local Similarity 79.3%; Pred. No. 1.9e+02;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 2 AATATGCTCTGTRTATATGCTATATGCT 30
DB 37056 AATATTCACCTGAGTGTCTCTATATGCT 37028
RESULT 10
ADH54712
ID ADH54712 standard; DNA; 59001 BP.
XX
XX ADH54712;
AC
XX
XX 25-MAR-2004 (first entry)
DT
XX
XX Human VEGF-C cDNA fragment #3.
DE
XX
XX human; ss; gene; VEGF-C; cardiovascular disorder; atherosclerosis;
KW diabetic retinopathy; autoimmune disorder; inflammatory disorder;
KW vascular endothelial growth factor.
XX
XX Homo sapiens.
OS
XX
XX US2003232437-A1.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 17-JUN-2002; 2002US-00173718.

XX
XX 17-JUN-2002; 2002US-00173718.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Zhang H, Dobie KW;
PI
XX
XX WPI; 2004-061284/06.
DR
XX
XX
XX New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding vascular endothelial growth factor-C (VEGF-C),
PT useful for treating atherosclerosis, diabetic retinopathy, or
PT inflammatory disorders.
XX
XX Example 15; SEQ ID NO 13; 83bp; English.
XX
XX The invention relates to a compound targeted to and which specifically
CC hybridizes with a nucleic acid molecule encoding VEGF-C, and inhibits the
CC expression of VEGF-C. The compound, composition and methods are useful
CC for treating a disease or condition associated with VEGF-C, such as a
CC cardiovascular disorder e.g. atherosclerosis or diabetic retinopathy or
CC an autoimmune or inflammatory disorder. They are also useful in research
CC and diagnostics for modulating the expression of VEGF-C. The present
CC sequence represents a human VEGF-C cDNA fragment.
XX
XX SQ Sequence 59001 BP; 17612 A; 10969 C; 10938 G; 19282 T; 0 U; 200 Other;
Query Match 68.7%; Score 20.6; DB 12; Length 59001;
Best Local Similarity 85.2%; Pred. No. 1.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 AATATGCTCTGTRTATATGCTATATG 28
DB 33098 AATATTCACCTGAGTGTCTCTATATG 33124
RESULT 11
ADL13501
ID ADL13501 standard; DNA; 167932 BP.
XX
XX ADL13501;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Osteoarthritis-associated polymorphic nucleotide #33.
DE
XX
XX ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW joint space narrowing; osteophyte development; joint pain;
KW osteoarthritis; SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
XX
XX WO2003054166-A2.
PN
XX
XX 03-JUL-2003.
PD
XX
XX 19-DEC-2002; 2002WO-US041225.
PF
XX
XX 20-DEC-2001; 2001US-0342603P.
PR
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX
XX Jones KA, Schafer A;
PI
XX
XX WPI; 2003-559141/52.
DR
XX
XX Determining susceptibility of an individual to joint space narrowing,
PT osteophyte development and/or joint pain comprises identifying whether
PT the individual has at least one polymorphism in a polynucleotide encoding
PT a protein.
XX
XX PS Disclosure; SEQ ID NO 33; 297bp; English.

CC The invention relates to a method of determining susceptibility of an
CC individual to joint space narrowing and/or osteophyte development and/or
CC joint pain comprising identifying whether the individual has at least one
CC polymorphism in a polynucleotide encoding at least one of the protein
CC listed in the specification. The methods, composition and agent are
CC useful for modulating the susceptibility of an individual to joint space
CC narrowing and/or osteophyte development and/or joint pain that is
CC associated with a disease, preferably osteoarthritis. The cell line and
CC the non-human animal are useful for screening for an agent for diagnosing
CC an individual having susceptibility to joint space narrowing and/or
CC osteophyte development and/or joint pain. This sequence corresponds to
CC the polynucleotide encoding a protein listed in the specification. (Note:
CC The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

CC
XX
SQ Sequence 167932 BP; 42550 A; 42808 C; 42441 G; 40130 T; 0 U; 3 Other;

Query Match 68.7%; Score 20.6; DB 10; Length 167932;
Best Local Similarity 79.3%; Pred. No. 2.1e+02;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AATATGCTGCTGTTATATGCTATATGCT 30
Db 47208 AATATTCACGTGCTGCTGCTATATGCT 47236

RESULT 12
ABLO5214
ID ABL05214 standard; cDNA; 4141 BP.
XX
AC ABL05214;
XX
DT 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 10124.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
OS WO200171042-A2.
XX
PN 27-SEP-2001.
XX
PD 23-MAR-2001; 2001WO-US009231.
XX
PF 23-MAR-2001; 2000US-0191637P.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
PA Venter JC, Adams M, Li PWD, Myers EW;
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
DR P-PSDB; ABB61111.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX
PS Claim 1; SEQ ID NO 10124; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 4164 BP; 982 A; 1023 C; 1048 G; 1088 T; 0 U; 0 Other;

Query Match 68.0%; Score 20.4; DB 4; Length 4164;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 ATATGCTGCTGTTATATGCTATAT 27
Db 252 ATATGCTCTATATATGCTGTA 275

RESULT 13
ABLO5338
ID ABL05338 standard; cDNA; 4164 BP.
XX
AC ABL05338;
XX
DT 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 10496.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
OS WO200171042-A2.
XX
PN 27-SEP-2001.
XX
PD 23-MAR-2001; 2001WO-US009231.
XX
PF 23-MAR-2000; 2000US-0191637P.
XX
PR 23-MAR-2000; 2000US-0191637P.
XX
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
PA Venter JC, Adams M, Li PWD, Myers EW;
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
DR P-PSDB; ABB61235.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX PT interactions.
XX
PS Claim 1; SEQ ID NO 10496; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

Qy 4 ATATGCTGCTGTTATATGCTATAT 27
Db 1990 ATATGCTCTATATATGCTGTA 2013

RESULT 14

Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TAAATAGCTCTGRTATATGCTATAT 27

Db 896 TCAATPACTCTGRTATATGCACTAT 922

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Job time : 433 secs

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OM nucleic - nucleic search, using sw model

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363.478 Million cell updates/sec

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Perfect score: 30
Sequence: 1 taaatagctctgtrtatatgcctatagtc 30

Scoring table: IDENTITY_NUC
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Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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18: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq: *
19: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq: *
20: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq: *
21: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq: *
22: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.2	74.0	78953	17	US-10-085-117-31
2	21.2	70.7	381	18	US-10-437-963-3640
3	21.2	70.7	1273	15	US-10-017-161-2339
4	21.2	70.7	1273	17	US-10-292-798-1985
5	20.8	69.3	42079	19	US-10-741-600-17960
6	20.8	69.3	260549	19	US-10-741-600-17723
7	20.6	68.7	1174	13	US-10-027-632-254267
8	20.6	68.7	1174	17	US-10-027-632-254267
9	20.6	68.7	59001	17	US-10-173-718-13
C 10	20.2	67.3	359	18	US-10-674-124A-12383
11	20.2	67.3	507	13	US-10-027-632-246790

12	20.2	67.3	507	13	US-10-027-632-246791	Sequence 246791,
13	20.2	67.3	507	17	US-10-027-632-246790	Sequence 246790,
14	20.2	67.3	507	17	US-10-027-632-246791	Sequence 246791,
15	20.2	67.3	2967	15	US-10-128-714-428	Sequence 428, App
16	20.2	67.3	3423	15	US-10-128-714-5428	Sequence 5428, App
17	20.2	67.3	15548	15	US-10-311-455-2128	Sequence 2128, App
C 18	20.2	67.3	86592	16	US-10-211-160-1	Sequence 1, Appl1
C 19	20.2	67.3	86592	16	US-10-051-681A-1	Sequence 17643, A
C 20	20.2	67.3	118356	18	US-10-741-601-17643	Sequence 17643, A
C 21	20.2	67.3	338287	19	US-10-741-601-5719	Sequence 5719, Ap
C 22	20.2	67.3	338287	19	US-10-741-600-17839	Sequence 17839, A
23	20	66.7	438	13	US-10-027-632-184011	Sequence 184011,
24	20	66.7	438	17	US-10-027-632-184011	Sequence 184011,
C 25	20	66.7	612	18	US-10-425-115-54267	Sequence 54267, A
C 26	20	66.7	45606	17	US-10-085-117-253	Sequence 253, App
C 27	19.8	66.0	1473	10	US-09-244-805-42	Sequence 42, Appl
C 28	19.8	66.0	1473	10	US-09-245-277-42	Sequence 42, Appl
C 29	19.8	66.0	1473	18	US-10-792-481-42	Sequence 72448, A
C 30	19.6	65.3	201	19	US-10-741-600-72448	Sequence 49282, A
C 31	19.6	65.3	264	17	US-10-242-535A-49282	Sequence 49282, A
C 32	19.6	65.3	264	17	US-10-085-783A-49282	Sequence 49282, A
C 33	19.6	65.3	377	17	US-10-242-535A-57512	Sequence 57512, A
C 34	19.6	65.3	377	17	US-10-085-783A-57512	Sequence 57512, A
C 35	19.6	65.3	384	9	US-09-960-352-4409	Sequence 4409, Ap
C 36	19.6	65.3	410	17	US-10-242-535A-23682	Sequence 23682, A
C 37	19.6	65.3	448	18	US-10-085-783A-23682	Sequence 23682, A
C 38	19.6	65.3	448	17	US-10-674-124A-1835	Sequence 14835, A
C 39	19.6	65.3	762	17	US-10-282-122A-1751	Sequence 15751, A
C 40	19.6	65.3	1024	17	US-10-260-238-1088	Sequence 1088, App
C 41	19.6	65.3	1475	18	US-09-873-367C-249	Sequence 249, App
C 42	19.6	65.3	1717	18	US-10-357-930-20223	Sequence 20223, A
C 43	19.6	65.3	1717	18	US-10-357-930-20223	Sequence 20223, A
C 44	19.6	65.3	1891	16	US-10-252-157-76	Sequence 26050, A
C 45	19.6	65.3	2076	9	US-09-822-849A-333	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-10-085-117-31/c
Sequence 31, Application US/10085117
Publication No. US20030232334A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 78953
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: variation
LOCATION: (1)...(78953)
OTHER INFORMATION: n = any nucleotide
US-10-085-117-31

Query Match 74.0%; Score 22.2; DB 17; Length 78953;
Best Local Similarity 82.8%; Pred. No. 1.1e+02;
Matches 24; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TAAATAGCTCTGTRTATATGCTATATGC 29
Db 12194 TCATTATAGCTCTGTRTATATGCTATATGC 12166

```
RESULT 2
US-10-437-963-3640
; Sequence 3640, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3640
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10597C.1
US-10-437-963-3640

Query Match      70.7%; Score 21.2; DB 18; Length 381;
Best Local Similarity 82.1%; Pred. No. 1.2e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 AATATGCTCTGTTATATGCTATATGCT 30
Db      343 AATATCTCTATATATCTGCTATATGCT 370

RESULT 3
US-10-017-161-2339
; Sequence 2339, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2339
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1073)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (445)..(544)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (597)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-2339
```

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Query Match      70.7%; Score 21.2; DB 15; Length 1273;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTTATATGCTATATG 28
Db      855 TATATATCTCTGTATATATATATATATG 882

RESULT 4
US-10-292-798-1985
; Sequence 1985, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 084335/166
; CURRENT APPLICATION NUMBER: US/10/292,798
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 10/017,161
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: JP 2001-246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2070
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1985
; LENGTH: 1273
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: source
; FEATURE:
; LOCATION: (1)..(1273)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1073)
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (445)..(544)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (597)..(597)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-1985

Query Match      70.7%; Score 21.2; DB 17; Length 1273;
Best Local Similarity 82.1%; Pred. No. 1.4e+02;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTTATATGCTATATG 28
Db      855 TATATATCTCTGTATATATATATATATG 882

RESULT 5
US-10-741-600-17906
; Sequence 17906, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17906
; LENGTH: 42079
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17906

Query Match
Best Local Similarity 69.3%; Score 20.8; DB 19; Length 42079;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATATGCTCTGRTATATGCTATAT 27
DB 35433 AATATGCTATATATATATGCTATAT 35458

RESULT 6
US-10-741-600-17723/C
; Sequence 17723, Application US/10741600
; Publication No. US2005026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: MOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17723
; LENGTH: 260549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17723

Query Match
Best Local Similarity 69.3%; Score 20.8; DB 19; Length 260549;
Matches 22; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATATGCTCTGRTATATGCTATAT 27
DB 141470 AATATGCTATATATATATGCTATAT 141445

RESULT 7
US-10-027-632-254267
; Sequence 254267, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254267
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-254267
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```

Query Match
Best Local Similarity 68.7%; Score 20.6; DB 13; Length 1174;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAAATGCTCTGRTATATGCTATATGC 29
DB 953 TAAAGTCTCTRTCTACATGCTGATGC 981

RESULT 8
US-10-027-632-254267
; Sequence 254267, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254267
; LENGTH: 1174
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-254267

Query Match
Best Local Similarity 79.3%; Score 20.6; DB 17; Length 1174;
Matches 23; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAAATGCTCTGRTATATGCTATATGC 29
DB 953 TAAAGTCTCTRTCTACATGCTGATGC 981

RESULT 9
US-10-173-718-13
; Sequence 13, Application US/10173718
; Publication No. US20030232437A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF VEGF-C EXPRESSION
; FILE REFERENCE: PTS-0036
; CURRENT APPLICATION NUMBER: US/10/173,718
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 125
; SEQ ID NO 13
; LENGTH: 59001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10057-10156
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
```

NAME/KEY: misc.feature
LOCATION: 53857-53956
OTHER INFORMATION: n = A,T,C or G
US-10-173-718-13

Query Match 68.7%; Score 20.6; DB 17; Length 59001;
Best Local Similarity 85.2%; Pred. No. 4.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAATATGCTCTGTATATGCTATATG 28
Db 33098 AAATATGCTCTGTATATGCTATATG 33124

RESULT 10
US-10-674-124A-12383/c
Sequence 12383, Application US/10674124A
Publication No. US20040197797A1
GENERAL INFORMATION:

APPLICANT: INOKO, Hidetoshi
APPLICANT: TAMURA, Gen
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
FILE REFERENCE: ORIN-003CIP
CURRENT APPLICATION NUMBER: US/10/674,124A
PRIOR FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: 10/257,511
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/JP00/07621
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: JP2000-112639
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: JP2002-327516
PRIOR FILING DATE: 2002-09-28
PRIOR APPLICATION NUMBER: JP2002-383869
PRIOR FILING DATE: 2002-12-09
NUMBER OF SEQ ID NOS: 27110
SEQ ID NO 12383
LENGTH: 359
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: AC004957.1_93436
FEATURE:
OTHER INFORMATION: Located on chromosome 7
FEATURE:
OTHER INFORMATION: Distance between a terminus base of telomere on
OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
FEATURE:
OTHER INFORMATION: sequence : 86314220
OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
OTHER INFORMATION: 5'-terminus of this base sequence : 6547
US-10-674-124A-12383

Query Match 67.3%; Score 20.2; DB 18; Length 359;
Best Local Similarity 81.5%; Pred. No. 2.9e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATATG 27
Db 137 TAAATATGCTCTGTATATGCTATATG 111

RESULT 11
US-10-027-632-246790
Sequence 246790, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108627.129

CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 246790
LENGTH: 507
TYPE: DNA
ORGANISM: Human
US-10-027-632-246790

Query Match 67.3%; Score 20.2; DB 13; Length 507;
Best Local Similarity 75.9%; Pred. No. 3e+02;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATATGC 29
Db 256 TAAATATGCTCTGTATATGCTATATGC 284

RESULT 12
US-10-027-632-246791
Sequence 246791, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 246791
LENGTH: 507
TYPE: DNA
ORGANISM: Human
US-10-027-632-246791

Query Match 67.3%; Score 20.2; DB 13; Length 507;
Best Local Similarity 75.9%; Pred. No. 3e+02;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TAAATATGCTCTGTATATGCTATATGC 29
Db 256 TAAATATGCTCTGTATATGCTATATGC 284

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RESULT 13
US-10-027-632-246790
; Sequence 246790, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246790
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-246790

Query Match      67.3%; Score 20.2; DB 17; Length 507;
Best Local Similarity 75.9%; Pred. No. 3e+02;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTRTATATGCTATATGC 29
Db      256 TAAATATTTTGTGAATTTCTGCTATATGC 284

RESULT 14
US-10-027-632-246791
; Sequence 246791, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246791
; LENGTH: 507
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-246791

Query Match      67.3%; Score 20.2; DB 17; Length 507;
Best Local Similarity 75.9%; Pred. No. 3e+02;
Matches 22; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTRTATATGCTATATGC 29
Db      256 TAAATATTTTGTGAATTTCTGCTATATGC 284

RESULT 15
US-10-128-714-428
; Sequence 428, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
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; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
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; PRIOR APPLICATION NUMBER: US 60/285,697
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; PRIOR APPLICATION NUMBER: US 60/287,066
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; PRIOR APPLICATION NUMBER: US 60/295,890
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; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 428
; LENGTH: 2967
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-428

Query Match      67.3%; Score 20.2; DB 15; Length 2967;
Best Local Similarity 81.5%; Pred. No. 4e+02;
Matches 22; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 TAAATATGCTCTGTRTATATGCTATAT 27
Db      441 TCAATATACTCTGTGATATATGCACTAT 467
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